SEQ ID NO. 1

```
          10         20         30         40
GACCAATCGGAGTGTGGTGAATTTTTGGAAAATATTTTGTGCGGTTCC
50         60         70         80         90
TTTAGTTGTGTAATATAGTACTTTAGTTACAAATTTGGAATAATTTGG
 100        110        120        130        140
CAGCAAAACCATCTGCAGCAACAAAATCATCTGCAGCTGCGAAATCAT
   150        160        170        180        190
CTGCAGCAGCAAAAGCATCTTCAGGAGCGAGAAAAGCCCCAAATAATG
          200        210        220
TGAG  ATG GCA GTT GAC GTC CGA ATC GCT GCC TTC
      Met Ala Val Asp Val Arg Ile Ala Ala Phe
  230        240        250        260
CTG CTG GTG TTT ATA GCG CCT GCA GTT TTA GCT CAA
Leu Leu Val Phe Ile Ala Pro Ala Val Leu Ala Gln
       270        280        290
GAG AGA TGT GGG TAT ATG ACC GCC ATC CCA AGG CTA
Glu Arg Cys Gly Tyr Met Thr Ala Ile Pro Arg Leu
300        310        320        330
 CCA CGA CCG GAT AAT TTG CCA GTA CTA AAT TTT GAA
 Pro Arg Pro Asp Asn Leu Pro Val Leu Asn Phe Glu
    340        350        360        370
GGC CAG ACA TGG AGT CAG AGG CCC CTG CTC CCC GCC
Gly Gln Thr Trp Ser Gln Arg Pro Leu Leu Pro Ala
          380        390        400
CCG GAG CGG GAT GAC CTG TGC ATG GAC GCC TAC CAC
Pro Glu Arg Asp Asp Leu Cys Met Asp Ala Tyr His
  410        420        430        440
GTG ATA ACA GCC AAC CTC GGC ACG CAG GTC ATC TAC
Val Ile Thr Ala Asn Leu Gly Thr Gln Val Ile Tyr
       450        460        470
ATG GAT GAA GAG ATA GAA GAC GAA ATC ACC ATC GCC
Met Asp Glu Glu Ile Glu Asp Glu Ile Thr Ile Ala
480        490        500        510
 ATA CTT AAT TAT AAC GGA CCA TCA ACT CCG TTC ATT
 Ile Leu Asn Tyr Asn Gly Pro Ser Thr Pro Phe Ile
```

FIG. 1A

```
                520                 530                 540                 550
GAA CTG CCA TTT TTA TCC GGT TCG TAC AAT CTG CTG
Glu Leu Pro Phe Leu Ser Gly Ser Tyr Asn Leu Leu
                560                 570                 580
ATG CCG GTC ATC AGG AGA GTT GAC AAC GGG GAG TGG
Met Pro Val Ile Arg Arg Val Asp Asn Gly Glu Trp
  590                 600                 610                 620
CAT CTC ATC ATC ACG CAA AGA CAG CAT TAC GAG TTG
His Leu Ile Ile Thr Gln Arg Gln His Tyr Glu Leu
                630                 640                 650
CCC GGC ATG CAG CAG TAC ATG TTC AAT GTG CGC GTG
Pro Gly Met Gln Gln Tyr Met Phe Asn Val Arg Val
660                 670                 680                 690
GAC GGC CAG TCG CTG GTG GCA GGC GTG TCT CTC GCT
Asp Gly Gln Ser Leu Val Ala Gly Val Ser Leu Ala
    700                 710                 720                 730
ATC GTC AAC ATA GAT GAC AAC GCG CCC ATC ATA CAA
Ile Val Asn Ile Asp Asp Asn Ala Pro Ile Ile Gln
                740                 750                 760
AAC TTC GAG CCT TGC CGG GTT CCT GAA CTG GGC GAG
Asn Phe Glu Pro Cys Arg Val Pro Glu Leu Gly Glu
  770                 780                 790                 800
CCA GGG TTG ACA GAA TGC ACA TAC CAA GTA TCG GAC
Pro Gly Leu Thr Glu Cys Thr Tyr Gln Val Ser Asp
                810                 820                 830
GCG GAC GGA CGG ATC AGC ACA GAG TTC ATG ACG TTC
Ala Asp Gly Arg Ile Ser Thr Glu Phe Met Thr Phe
840                 850                 860                 870
AGG ATC GAC AGC GTT CGT GGC GAC GAG GAG ACC TTC
Arg Ile Asp Ser Val Arg Gly Asp Glu Glu Thr Phe
    880                 890                 900                 910
TAC ATC GAA CGG ACG AAT ATC CCC AAC CAA TGG ATG
Tyr Ile Glu Arg Thr Asn Ile Pro Asn Gln Trp Met
                920                 930                 940
TGG CTA AAT ATG ACC ATA GGC GTT AAT ACC TCG CTC
Trp Leu Asn Met Thr Ile Gly Val Asn Thr Ser Leu
```

FIG. 1B

```
                                                                  980
                950                 960                 970
AAC TTC GTC ACC AGT CCG CTG CAT ATA TTC AGC GTG
Asn Phe Val Thr Ser Pro Leu His Ile Phe Ser Val
                990                1000                1010
ACA GCC CTG GAC TCG CTC CCG AAC ACC CAC ACG GTG
Thr Ala Leu Asp Ser Leu Pro Asn Thr His Thr Val
1020                1030                1040                1050
  ACT ATG ATG GTG CAA GTG GCG AAT GTG AAC AGC
  Thr Met Met Val Gln Val Ala Asn Val Asn Ser
                1060                1070                1080
CGT CCG CCG CGC TGG CTG GAG ATC TTC GCT GTC CAA
Arg Pro Pro Arg Trp Leu Glu Ile Phe Ala Val Gln
1090                1100                1110                1120
  CAG TTT GAA GAG AAA TCT TAC CAA AAC TTC ACA
  Gln Phe Glu Glu Lys Ser Tyr Gln Asn Phe Thr
                1130                1140                1150
GTG AGG GCG ATC GAC GGA GAC ACT GAG ATC AAT ATG
Val Arg Ala Ile Asp Gly Asp Thr Glu Ile Asn Met
1160                1170                1180                1190
CCT ATC AAC TAC AGG CTG ATC ACA AAT GAG GAA GAC
Pro Ile Asn Tyr Arg Leu Ile Thr Asn Glu Glu Asp
                1200                1210                1220
ACA TTC TTC AGC ATT GAG GCC CTG CCT GGT GGA AAA
Thr Phe Phe Ser Ile Glu Ala Leu Pro Gly Gly Lys
1230                1240                1250                1260
  AGC GGG GCT GTA TTC CTC GTG TCG CCA ATT GAC
  Ser Gly Ala Val Phe Leu Val Ser Pro Ile Asp
                1270                1280                1290
CGC GAC ACA CTG CAA CGA GAG GTG TTT CCA CTT ACG
Arg Asp Thr Leu Gln Arg Glu Val Phe Pro Leu Thr
1300                1310                1320                1330
  ATC GTC GCT TAC AAA TAT GAT GAG GAG GCC TTC TCC
  Ile Val Ala Tyr Lys Tyr Asp Glu Glu Ala Phe Ser
                1340                1350                1360
ACA TCA ACA AAC GTG GTC ATC ATT GTG ACA GAC ATC
Thr Ser Thr Asn Val Val Ile Ile Val Thr Asp Ile
```

FIG. 1C

```
1370          1380          1390          1400
   AAC GAC CAA AGA CCT GAA CCT ATA CAC AAG GAA
   Asn Asp Gln Arg Pro Glu Pro Ile His Lys Glu
      1410          1420          1430
TAT CGA CTG GCA ATC ATG GAG GAG ACG CCC CTG ACC
Tyr Arg Leu Ala Ile Met Glu Glu Thr Pro Leu Thr
1440          1450          1460          1470
   CTC AAC TTC GAT AAA GAA TTC GGA TTT CAT GAT
   Leu Asn Phe Asp Lys Glu Phe Gly Phe His Asp
         1480          1490          1500
AAG GAT TTA GGT CAA AAC GCT CAG TAC ACG GTG CGT
Lys Asp Leu Gly Gln Asn Ala Gln Tyr Thr Val Arg
1510          1520          1530          1540
   CTA GAG AGC GTG GAC CCT CCA GGC GCT GCT GAG GCA
   Leu Glu Ser Val Asp Pro Pro Gly Ala Ala Glu Ala
         1550          1560          1570
TTC TAC ATA GCG CCT GAA GTC GGC TAC CAG CGA CAG
Phe Tyr Ile Ala Pro Glu Val Gly Tyr Gln Arg Gln
1580          1590          1600          1610
   ACC TTC ATC ATG GGC ACC CTC AAT CAC TCC ATG
   Thr Phe Ile Met Gly Thr Leu Asn His Ser Met
      1620          1630          1640
CTG GAT TAC GAA GTG CCA GAG TTT CAG AGT ATT ACG
Leu Asp Tyr Glu Val Pro Glu Phe Gln Ser Ile Thr
1650          1660          1670          1680
   ATT CGG GTG GTA GCG ACC GAC AAC AAC GAC ACG
   Ile Arg Val Val Ala Thr Asp Asn Asn Asp Thr
         1690          1700          1710
AGG CAC GTG GGC GTC GCG TTG GTT CAC ATT GAC CTC
Arg His Val Gly Val Ala Leu Val His Ile Asp Leu
1720          1730          1740          1750
   ATC AAT TGG AAC GAT GAG CAG CCG ATC TTC GAA CAC
   Ile Asn Trp Asn Asp Glu Gln Pro Ile Phe Glu His
         1760          1770          1780
GCC GTG CAG ACC GTC ACC TTC GAC GAG ACT GAA GGC
Ala Val Gln Thr Val Thr Phe Asp Glu Thr Glu Gly
```

FIG. 1D

```
1790          1800          1810          1820
   GAG GGG TTC TTC GTC GCC AAG GCG GTT GCA CAC
   Glu Gly Phe Phe Val Ala Lys Ala Val Ala His
      1830          1840          1850
GAC AGA GAC ATC GGG GAT GTC GTC GAG CAT ACT TTA
Asp Arg Asp Ile Gly Asp Val Val Glu His Thr Leu
1860          1870          1880          1890
  TTG GGT AAC GCT GTT AAC TTC CTG ACC ATC GAC
  Leu Gly Asn Ala Val Asn Phe Leu Thr Ile Asp
        1900          1910          1920
AAA CTC ACC GGC GAC ATC CGC GTC TCA GCT AAC GAC
Lys Leu Thr Gly Asp Ile Arg Val Ser Ala Asn Asp
1930          1940          1950          1960
 TCC TTC AAC TAC CAT CGA GAA AGT GAA TTA TTT GTG
 Ser Phe Asn Tyr His Arg Glu Ser Glu Leu Phe Val
      1970          1980          1990
CAG GTG CGA GCT ACA GAC ACG CTG GGC GAA CCC TTC
Gln Val Arg Ala Thr Asp Thr Leu Gly Glu Pro Phe
2000          2010          2020          2030
   CAC ACG GCG ACG TCA CAG CTG GTC ATA CGA CTA
   His Thr Ala Thr Ser Gln Leu Val Ile Arg Leu
      2040          2050          2060
AAT GAC ATC AAC AAC ACG CCA CCC ACC TTA CGG CTG
Asn Asp Ile Asn Asn Thr Pro Pro Thr Leu Arg Leu
2070          2080          2090          2100
  CCT CGA GGC AGT CCC CAA GTG GAG GAG AAC GTG
  Pro Arg Gly Ser Pro Gln Val Glu Glu Asn Val
        2110          2120          2130
CCT GAT GGC CAC GTC ATC ACC CAG GAG TTA CGC GCC
Pro Asp Gly His Val Ile Thr Gln Glu Leu Arg Ala
2140          2150          2160          2170
 ACC GAC CCC GAC ACC ACG GCC GAT CTG CGC TTC GAG
 Thr Asp Pro Asp Thr Thr Ala Asp Leu Arg Phe Glu
      2180          2190          2200
ATA AAC TGG GAC ACC TCT TTC GCC ACC AAG CAA GGC
Ile Asn Trp Asp Thr Ser Phe Ala Thr Lys Gln Gly
```

FIG. 1E

```
2210          2220          2230          2240
   CGC CAG GCT AAC CCC GAC GAG TTT AGG AAT TGC
   Arg Gln Ala Asn Pro Asp Glu Phe Arg Asn Cys
      2250          2260          2270
GTG GAA ATC GAG ACC ATC TTC CCC GAG ATT AAC AAC
Val Glu Ile Glu Thr Ile Phe Pro Glu Ile Asn Asn
2280          2290          2300          2310
  CGG GGA CTG GCT ATC GGC CGC GTT GTA GCG CGC
  Arg Gly Leu Ala Ile Gly Arg Val Val Ala Arg
       2320          2330          2340
GAA ATC AGA CAC AAC GTG ACC ATA GAC TAC GAG GAG
Glu Ile Arg His Asn Val Thr Ile Asp Tyr Glu Glu
2350          2360          2370          2380
 TTT GAG GTC CTC TCC CTC ACA GTG AGG GTG CGT GAC
 Phe Glu Val Leu Ser Leu Thr Val Arg Val Arg Asp
      2390          2400          2410
CTT AAC ACC GTC TAC GGA GAC GAC TAC GAC GAA TCG
Leu Asn Thr Val Tyr Gly Asp Asp Tyr Asp Glu Ser
2420          2430          2440          2450
   ATG CTC ACA ATA ACT ATA ATC GAT ATG AAC GAC
   Met Leu Thr Ile Thr Ile Ile Asp Met Asn Asp
      2460          2470          2480
AAC GCG CCG GTG TGG GTG GAG GGG ACT CTG GAG CAG
Asn Ala Pro Val Trp Val Glu Gly Thr Leu Glu Gln
2490          2500          2510          2520
  AAC TTC CGA GTC CGC GAG ATG TCG GCG GGC GGG
  Asn Phe Arg Val Arg Glu Met Ser Ala Gly Gly
       2530          2540          2550
CTC GTG GTG GGC TCC GTG CGC GCG GAC GAC ATC GAC
Leu Val Val Gly Ser Val Arg Ala Asp Asp Ile Asp
2560          2570          2580          2590
 GGA CCG CTC TAC AAC CAA GTG CGA TAC ACC ATT TTC
 Gly Pro Leu Tyr Asn Gln Val Arg Tyr Thr Ile Phe
      2600          2610          2620
CCT CGT GAA GAC ACA GAT AAG GAC CTG ATA ATG ATC
Pro Arg Glu Asp Thr Asp Lys Asp Leu Ile Met Ile
```

FIG. 1F

```
2630          2640          2650          2660
   GAC TTC CTC ACG GGT CAA ATT TCC GTG AAC ACA
   Asp Phe Leu Thr Gly Gln Ile Ser Val Asn Thr
      2670          2680          2690
AGC GGC GCC ATC GAC GCG GAT ACT CCT CCA CGC TTC
Ser Gly Ala Ile Asp Ala Asp Thr Pro Pro Arg Phe
2700          2710          2720          2730
   CAC CTC TAC TAT ACA GTG GTC GCT AGT GAC CGA
   His Leu Tyr Tyr Thr Val Val Ala Ser Asp Arg
        2740          2750          2760
TGC TCG ACA GAA GAT CCT GCA GAT TGC CCC CCT GAC
Cys Ser Thr Glu Asp Pro Ala Asp Cys Pro Pro Asp
2770          2780          2790          2800
 CCG ACT TAT TGG GAA ACC GAA GGA AAT ATC ACA ATC
 Pro Thr Tyr Trp Glu Thr Glu Gly Asn Ile Thr Ile
      2810          2820          2830
CAC ATC ACC GAC ACG AAC AAC AAG GTC CCG CAG GCG
His Ile Thr Asp Thr Asn Asn Lys Val Pro Gln Ala
2840          2850          2860          2870
   GAA ACG ACT AAG TTC GAT ACC GTC GTG TAT ATT
   Glu Thr Thr Lys Phe Asp Thr Val Val Tyr Ile
      2880          2890          2900
TAC GAG AAC GCA ACC CAC TTA GAC GAG GTG GTC ACT
Tyr Glu Asn Ala Thr His Leu Asp Glu Val Val Thr
2910          2920          2930          2940
   CTG ATA GCC AGT GAT CTT GAC AGA GAC GAA ATA
   Leu Ile Ala Ser Asp Leu Asp Arg Asp Glu Ile
        2950          2960          2970
TAC CAC ACG GTG AGC TAC GTC ATC AAT TAT GCA GTG
Tyr His Thr Val Ser Tyr Val Ile Asn Tyr Ala Val
2980          2990          3000          3010
 AAC CCT CGA CTG ATG AAC TTC TTC TCC GTG AAC CGA
 Asn Pro Arg Leu Met Asn Phe Phe Ser Val Asn Arg
      3020          3030          3040
GAG ACC GGC CTG GTG TAC GTG GAC TAT GAG ACC CAG
Glu Thr Gly Leu Val Tyr Val Asp Tyr Glu Thr Gln
```

FIG. 1G

```
3050          3060          3070          3080
   GGT AGT GGC GAG GTG CTG GAC CGT GAT GGT GAT
   Gly Ser Gly Glu Val Leu Asp Arg Asp Gly Asp
      3090          3100          3110
GAA CCA ACG CAC CGT ATC TTC TTC AAC CTC ATC GAC
Glu Pro Thr His Arg Ile Phe Phe Asn Leu Ile Asp
3120          3130          3140          3150
  AAC TTC ATG GGG GAA GGA GAA GGT AAC AGA AAT
  Asn Phe Met Gly Glu Gly Glu Gly Asn Arg Asn
        3160          3170          3180
CAG AAC GAC ACA GAA GTT CTC GTT ATC TTG TTG GAT
Gln Asn Asp Thr Glu Val Leu Val Ile Leu Leu Asp
3190          3200          3210          3220
 GTG AAT GAC AAT GCT CCT GAA TTG CCA CCG CCG AGC
 Val Asn Asp Asn Ala Pro Glu Leu Pro Pro Pro Ser
      3230          3240          3250
GAA CTC TCT TGG ACT ATA TCT GAG AAC CTT AAG CAG
Glu Leu Ser Trp Thr Ile Ser Glu Asn Leu Lys Gln
3260          3270          3280          3290
   GGC GTC CGT CTT GAA CCA CAT ATC TTC GCC CCG
   Gly Val Arg Leu Glu Pro His Ile Phe Ala Pro
      3300          3310          3320
GAC CGC GAC GAG CCC GAC ACA GAC AAC TCC AGG GTC
Asp Arg Asp Glu Pro Asp Thr Asp Asn Ser Arg Val
3330          3340          3350          3360
  GGC TAC GAG ATC CTG AAC CTC AGC ACG GAG CGG
  Gly Tyr Glu Ile Leu Asn Leu Ser Thr Glu Arg
        3370          3380          3390
GAC ATC GAA GTG CCG GAG CTG TTT GTG ATG ATA CAG
Asp Ile Glu Val Pro Glu Leu Phe Val Met Ile Gln
3400          3410          3420          3430
 ATC GCG AAC GTC ACG GGA GAG CTG GAG ACC GCC ATG
 Ile Ala Asn Val Thr Gly Glu Leu Glu Thr Ala Met
      3440          3450          3460
GAC CTC AAG GGA TAT TGG GGG ACG TAC GCT ATA CAT
Asp Leu Lys Gly Tyr Trp Gly Thr Tyr Ala Ile His
```

FIG. 1H

```
                                                                3500
3470            3480            3490
   ATA CGG GCA TTC GAC CAC GGC ATT CCG CAA ATG
   Ile Arg Ala Phe Asp His Gly Ile Pro Gln Met
      3510            3520            3530
TCC ATG AAC GAG ACA TAT GAG CTG ATC ATC CAT CCG
Ser Met Asn Glu Thr Tyr Glu Leu Ile Ile His Pro
3540            3550            3560            3570
  TTC AAC TAC TAC GCG CCT GAG TTC GTC TTC CCG
  Phe Asn Tyr Tyr Ala Pro Glu Phe Val Phe Pro
        3580            3590            3600
ACC AAC GAT GCC GTC ATA CGA CTT GCG AGG GAA CGA
Thr Asn Asp Ala Val Ile Arg Leu Ala Arg Glu Arg
3610            3620            3630            3640
 GCT GTA ATC AAT GGA GTT CTA GCG ACA GTG AAC GGA
 Ala Val Ile Asn Gly Val Leu Ala Thr Val Asn Gly
      3650            3660            3670
GAG TTC TTG GAG CGG ATA TCG GCG ACT GAT CCG GAC
Glu Phe Leu Glu Arg Ile Ser Ala Thr Asp Pro Asp
3680            3690            3700            3710
   GGA CTC CAC GCG GGC GTC GTC ACC TTC CAA GTG
   Gly Leu His Ala Gly Val Val Thr Phe Gln Val
      3720            3730            3740
GTA GGC GAT GAG GAA TCA CAA CGG TAC TTT CAA GTA
Val Gly Asp Glu Glu Ser Gln Arg Tyr Phe Gln Val
3750            3760            3770            3780
  GTT AAC GAT GGC GAG AAC CTC GGC TCG TTG AGG
  Val Asn Asp Gly Glu Asn Leu Gly Ser Leu Arg
        3790            3800            3810
TTA CTG CAA GCC GTT CCA GAG GAG ATC AGG GAG TTC
Leu Leu Gln Ala Val Pro Glu Glu Ile Arg Glu Phe
3820            3830            3840            3850
 CGG ATA ACG ATT CGC GCT ACA GAC CAG GGA ACG GAC
 Arg Ile Thr Ile Arg Ala Thr Asp Gln Gly Thr Asp
      3860            3870            3880
CCA GGA CCG CTG TCC ACG GAC ATG ACG TTC AGA GTT
Pro Gly Pro Leu Ser Thr Asp Met Thr Phe Arg Val
```

FIG. 11

```
                                                                3920
3890          3900          3910
   GTT TTT GTG CCC ACG CAA GGA GAA CCT AGA TTC
   Val Phe Val Pro Thr Gln Gly Glu Pro Arg Phe
      3930          3940          3950
GCG TCC TCA GAA CAT GCT GTC GCT TTC ATA GAA AAG
Ala Ser Ser Glu His Ala Val Ala Phe Ile Glu Lys
                                                3990
3960          3970          3980
   AGT GCC GGC ATG GAA GAG TCT CAC CAA CTT CCT
   Ser Ala Gly Met Glu Glu Ser His Gln Leu Pro
        4000          4010          4020
CTA GCA CAA GAC ATC AAG AAC CAT CTC TGT GAA GAC
Leu Ala Gln Asp Ile Lys Asn His Leu Cys Glu Asp
                                                4060
4030          4040          4050
   GAC TGT CAC AGC ATT TAC TAT CGT ATT ATC GAT GGC
   Asp Cys His Ser Ile Tyr Tyr Arg Ile Ile Asp Gly
        4070          4080          4090
AAC AGC GAA GGT CAT TTC GGC CTG GAT CCT GTT CGC
Asn Ser Glu Gly His Phe Gly Leu Asp Pro Val Arg
                                                4130
4100          4110          4120
      AAC AGG TTG TTC CTG AAG AAA GAG CTG ATA AGG
      Asn Arg Leu Phe Leu Lys Lys Glu Leu Ile Arg
           4140          4150          4160
GAA CAA AGT GCC TCC CAC ACT CTG CAA GTG GCG GCT
Glu Gln Ser Ala Ser His Thr Leu Gln Val Ala Ala
                                                4200
4170          4180          4190
   AGT AAC TCG CCC GAT GGT GGC ATT CCA CTT CCT
   Ser Asn Ser Pro Asp Gly Gly Ile Pro Leu Pro
        4210          4220          4230
GCT TCC ATC CTT ACT GTC ACT GTT ACC GTG AGG GAG
Ala Ser Ile Leu Thr Val Thr Val Thr Val Arg Glu
                                                4270
4240          4250          4260
   GCA GAC CCT CGT CCA GTG TTT GTG AGG GAA TTG TAC
   Ala Asp Pro Arg Pro Val Phe Val Arg Glu Leu Tyr
        4280          4290          4300
ACC GCA GGG ATA TCC ACA GCG GAC TCC ATC GGC AGA
Thr Ala Gly Ile Ser Thr Ala Asp Ser Ile Gly Arg
```

FIG. 1J

```
                                                  4330                4340
4310              4320
   GAG CTG CTC AGA TTA CAT GCG ACC CAG TCT GAA
   Glu Leu Leu Arg Leu His Ala Thr Gln Ser Glu
      4350              4360                4370
GGC TCG GCC ATT ACT TAT GCT ATA GAC TAC GAT ACA
Gly Ser Ala Ile Thr Tyr Ala Ile Asp Tyr Asp Thr
                                    4400                4410
4380              4390
   ATG GTA GTG GAC CCC AGC CTG GAG GCA GTG AGA
   Met Val Val Asp Pro Ser Leu Glu Ala Val Arg
         4420              4430                4440
CAG TCG GCT TTC GTA CTG AAC GCT CAA ACC GGA GTG
Gln Ser Ala Phe Val Leu Asn Ala Gln Thr Gly Val
                                    4470                4480
4450              4460
   CTG ACG CTT AAT ATC CAG CCC ACG GCC ACG ATG CAT
   Leu Thr Leu Asn Ile Gln Pro Thr Ala Thr Met His
         4490              4500                4510
GGA CTG TTC AAA TTC GAA GTC ACA GCT ACT GAC ACG
Gly Leu Phe Lys Phe Glu Val Thr Ala Thr Asp Thr
                                    4540                4550
4520              4530
      GCC GGC GCT CAG GAC CGC ACC GAC GTC ACC GTG
      Ala Gly Ala Gln Asp Arg Thr Asp Val Thr Val
         4560              4570                4580
TAC GTG GTA TCC TCG CAG AAC CGC GTC TAC TTC GTG
Tyr Val Val Ser Ser Gln Asn Arg Val Tyr Phe Val
                                    4610                4620
4590              4600
   TTC GTC AAC ACG CTG CAA CAG GTC GAA GAC AAC
   Phe Val Asn Thr Leu Gln Gln Val Glu Asp Asn
         4630              4640                4650
AGA GAC TTT ATC GCG GAC ACC TTC AGC GCT GGG TTC
Arg Asp Phe Ile Ala Asp Thr Phe Ser Ala Gly Phe
                                    4680                4690
4660              4670
   AAC ATG ACC TGC AAC ATC GAC CAA GTG GTG CCC GCT
   Asn Met Thr Cys Asn Ile Asp Gln Val Val Pro Ala
         4700              4710                4720
AAC GAC CCC GTC ACC GGC GTG GCG CTG GAG CAC AGC
Asn Asp Pro Val Thr Gly Val Ala Leu Glu His Ser
```

FIG. 1K

```
4730        4740        4750        4760
   ACG CAG ATG CGC GGC CAC TTC ATA CGG GAC AAC
   Thr Gln Met Arg Gly His Phe Ile Arg Asp Asn
      4770        4780        4790
GTA CCC GTA CTC GCT GAT GAG ATA GAA CAG ATC CGT
Val Pro Val Leu Ala Asp Glu Ile Glu Gln Ile Arg
4800        4810        4820        4830
   AGT GAC CTA GTC CTC CTG AGC TCG ATA CAA ACA
   Ser Asp Leu Val Leu Leu Ser Ser Ile Gln Thr
        4840        4850        4860
ACG CTG GCG GCG CGA TCG CTG GTG TTG CAG GAC TTG
Thr Leu Ala Ala Arg Ser Leu Val Leu Gln Asp Leu
4870        4880        4890        4900
   TTG ACC AAC TCC AGC CCG GAC TCG GCG CCT GAC TCG
   Leu Thr Asn Ser Ser Pro Asp Ser Ala Pro Asp Ser
        4910        4920        4930
AGC CTC ACG GTG TAC GTG CTG GCC TCA CTG TCT GCT
Ser Leu Thr Val Try Val Leu Ala Ser Leu Ser Ala
4940        4950        4960        4970
   GTG CTC GGT TTC ATG TGC CTT GTG CTA CTG CTT
   Val Leu Gly Phe Met Cys Leu Val Leu Leu Leu
      4980        4990        5000
ACC TTC ATC ATC AGG ACT AGA GCG CTA AAC CGA CGG
Thr Phe Ile Ile Arg Thr Arg Ala Leu Asn Arg Arg
5010        5020        5030        5040
   TTG GAA GCC CTG TCG ATG ACG AAG TAC GGC TCA
   Leu Glu Ala Leu Ser Met Thr Lys Tyr Gly Ser
        5050        5060        5070
CTG GAC TCT GGA TTG AAC CGC GCC GGC ATC GCC GCC
Leu Asp Ser Gly Leu Asn Arg Ala Gly Ile Ala Ala
5080        5090        5100        5110
   CCC GGC ACC AAC AAA CAC ACT GTG GAA GGC TCC AAC
   Pro Gly Thr Asn Lys His Thr Val Glu Gly Ser Asn
        5120        5130        5140
CCT ATC TTC AAT GAA GCA ATA AAG ACG CCA GAT TTA
Pro Ile Phe Asn Glu Ala Ile Lys Thr Pro Asp Leu
```

FIG. 1L

```
5150          5160          5170          5180
   GAT GCC ATT AGC GAG GGT TCC AAC GAC TCT GAT
   Asp Ala Ile Ser Glu Gly Ser Asn Asp Ser Asp
      5190          5200          5210
CTG ATC GGC ATC GAA GAT CTT CCG CAC TTT GGC AAC
Leu Ile Gly Ile Glu Asp Leu Pro His Phe Gly Asn
5220          5230          5240          5250
  GTC TTC ATG GAT CCT GAG GTG AAC GAA AAG GCA
  Val Phe Met Asp Pro Glu Val Asn Glu Lys Ala
        5260          5270          5280
AAT GGT TAT CCC GAA GTC GCA AAC CAC AAC AAC AAC
Asn Gly Tyr Pro Glu Val Ala Asn His Asn Asn Asn
5290          5300          5310          5320
 TTC GCT TTC AAC CCG ACT CCC TTC TCG CCT GAG TTC
 Phe Ala Phe Asn Pro Thr Pro Phe Ser Pro Glu Phe
      5330          5340          5350          5360
GTT AAC GGA CAG TTC AGA AAG ATC TAGAAGATAACAACA
Val Asn Gly Gln Phe Arg Lys Ile
   5370          5380          5390          5400          5410
CTAGTTAAGATCATTAATTTTGGAGTTTGGAATTAAGATTTTTGAAAG
         5420          5430          5440          5450
GATAGTTGTGATAAGCCTGTGATTTTTAAAACTGTAATTGAAAAAA
5460          5470          5480          5490          5500
AAAATTGAGACCTCCATTTAAGCTCTTGCTCTCATCTCATCAAATTTT
   5510          5520          5530          5540          5550
ATAAAATGCCATTAGTCATTAAGATACTCGATTTAATTTAAGATTATT
      5560          5570          5580
TAAGATATTATGTAAAATAAATATATTGTC
```

FIG. 1M

SEQ ID NO. 2

```
Met Ala Val Asp Val Arg Ile Ala Ala Phe Leu Leu
 1               5                  10
Val Phe Ile Ala Pro Ala Val Leu Ala Gln Glu Arg
            15                  20
Cys Gly Tyr Met Thr Ala Ile Pro Arg Leu Pro Arg
        25                  30                  35
Pro Asp Asn Leu Pro Val Leu Asn Phe Glu Gly Gln
                40                  45
Thr Trp Ser Gln Arg Pro Leu Leu Pro Ala Pro Glu
    50                  55                  60
```

CAD1

```
Arg Asp Asp Leu Cys Met Asp Ala Tyr His Val Ile
                65                  70
Thr Ala Asn Leu Gly Thr Gln Val Ile Tyr Met Asp
            75                  80
Glu Glu Ile Glu Asp Glu Ile Thr Ile Ala Ile Leu
        85                  90                  95
Asn Tyr Asn Gly Pro Ser Thr Pro Phe Ile Glu Leu
                100                 105
Pro Phe Leu Ser Gly Ser Tyr Asn Leu Leu Met Pro
    110                 115                 120
Val Ile Arg Arg Val Asp Asn Gly Glu Trp His Leu
                125                 130
Ile Ile Thr Gln Arg Gln His Tyr Glu Leu Pro Gly
            135                 140
Met Gln Gln Tyr Met Phe Asn Val Arg Val Asp Gly
        145                 150                 155
Gln Ser Leu Val Ala Gly Val Ser Leu Ala Ile Val
                160                 165
```

CAD2

```
Asn Ile Asp Asp Asn Ala Pro Ile Ile Gln Asn Phe
    170                 175                 180
Glu Pro Cys Arg Val Pro Glu Leu Gly Glu Pro Gly
                185                 190
Leu Thr Glu Cys Thr Tyr Gln Val Ser Asp Ala Asp
            195                 200
Gly Arg Ile Ser Thr Glu Phe Met Thr Phr Arg Ile
        205                 210                 215
```

FIG. 2A

```
Asp Ser Val Arg Gly Asp Glu Glu Thr Phe Tyr Ile
          220                 225
Glu Arg Thr Asn Ile Pro Asn Gln Trp Met Trp Leu
    230                 235                 240
Asn Met Thr Ile Gly Val Asn Thr Ser Leu Asn Phe
                245                 250
Val Thr Ser Pro Leu His Ile Phe Ser Val Thr Ala
          255                 260
Leu Asp Ser Leu Pro Asn Thr His Thr Val Thr Met
265                 270                 275
Met Val Gln Val Ala Asn Val Asn Ser Arg Pro Pro
          280                 285
          CAD3
Arg Trp Leu Glu Ile Phe Ala Val Gln Gln Phe Glu
    290                 295                 300
Glu Lys Ser Tyr Gln Asn Phe Thr Val Arg Ala Ile
                305                 310
Asp Gly Asp Thr Glu Ile Asn Met Pro Ile Asn Tyr
          315                 320
Arg Leu Ile Thr Asn Glu Glu Asp Thr Phe Phe Ser
325                 330                 335
Ile Glu Ala Leu Pro Gly Gly Lys Ser Gly Ala Val
          340                 345
Phe Leu Val Ser Pro Ile Asp Arg Asp Thr Leu Gln
    350                 355                 360
Arg Glu Val Phe Pro Leu Thr Ile Val Ala Tyr Lys
                365                 370
Tyr Asp Glu Glu Ala Phe Ser Thr Ser Thr Asn Val
          375                 380
Val Ile Ile Val Thr Asp Ile Asn Asp Gln Arg Pro
385                 390                 395
     CAD4
Glu Pro Ile His Lys Glu Tyr Arg Leu Ala Ile Met
          400                 405
Glu Glu Thr Pro Leu Thr Leu Asn Phe Asp Lys Glu
    410                 415                 420
Phe Gly Phe His Asp Lys Asp Leu Gly Gln Asn Ala
                425                 430
```

FIG. 2B

```
Gln Tyr Thr Val Arg Leu Glu Ser Val Asp Pro Pro
        435                 440
Gly Ala Ala Glu Ala Phe Tyr Ile Ala Pro Glu Val
445                 450                 455
Gly Tyr Gln Arg Gln Thr Phe Ile Met Gly Thr Leu
            460                 465
Asn His Ser Met Leu Asp Tyr Glu Val Pro Glu Phe
    470                 475                 480
Gln Ser Ile Thr Ile Arg Val Val Ala Thr Asp Asn
                485         |CAD5--> 490
Asn Asp Thr Arg His Val Gly Val Ala Leu Val His
        495                 500
Ile Asp Leu Ile Asn Trp Asn Asp Glu Gln Pro Ile
505                 510                 515
Phe Glu His Ala Val Gln Thr Val Thr Phe Asp Glu
            520                 525
Thr Glu Gly Glu Gly Phe Phe Val Ala Lys Ala Val
    530                 535                 540
Ala His Asp Arg Asp Ile Gly Asp Val Val Glu His
                545                 550
Thr Leu Leu Gly Asn Ala Val Asn Phe Leu Thr Ile
        555                 560
Asp Lys Leu Thr Gly Asp Ile Arg Val Ser Ala Asn
565                 570                 575
Asp Ser Phe Asn Tyr His Arg Glu Ser Glu Leu Phe
            580                 585
Val Gln Val Arg Ala Thr Asp Thr Leu Gly Glu Pro
    590                 595                 600
Phe His Thr Ala Thr Ser Gln Leu Val Ile Arg Leu
                605                 610     |CAD6
Asn Asp Ile Asn Asn Thr Pro Pro Thr Leu Arg Leu
-->     615                 620
Pro Arg Gly Ser Pro Gln Val Glu Glu Asn Val Pro
625                 630                 635
Asp Gly His Val Ile Thr Gln Glu Leu Arg Ala Thr
            640                 645
```

FIG. 2C

```
Asp Pro Asp Thr Thr Ala Asp Leu Arg Phe Glu Ile
650                 655                 660
Asn Trp Asp Thr Ser Phe Ala Thr Lys Gln Gly Arg
                665                 670
Gln Ala Asn Pro Asp Glu Phe Arg Asn Cys Val Glu
        675                 680
Ile Glu Thr Ile Phe Pro Glu Ile Asn Asn Arg Gly
685                 690                 695
Leu Ala Ile Gly Arg Val Val Ala Arg Glu Ile Arg
            700                 705
His Asn Val Thr Ile Asp Tyr Glu Glu Phe Glu Val
710                 715                 720
Leu Ser Leu Thr Val Arg Val Arg Asp Leu Asn Thr
                725                 730
Val Tyr Gly Asp Asp Tyr Asp Glu Ser Met Leu Thr
        735                 740
Ile Thr Ile Ile Asp Met Asn Asp Asn Ala Pro Val
745                 750                 755
Trp Val Glu Gly Thr Leu Glu Gln Asn Phe Arg Val
            760                 765
Arg Glu Met Ser Ala Gly Gly Leu Val Val Gly Ser
770                 775                 780
Val Arg Ala Asp Asp Ile Asp Gly Pro Leu Tyr Asn
                785                 790
Gln Val Arg Tyr Thr Ile Phe Pro Arg Glu Asp Thr
        795                 800
Asp Lys Asp Leu Ile Met Ile Asp Phe Leu Thr Gly
805                 810                 815
Gln Ile Ser Val Asn Thr Ser Gly Ala Ile Asp Ala
            820                 825
Asp Thr Pro Pro Arg Phe His Leu Tyr Tyr Thr Val
830                 835                 840
Val Ala Ser Asp Arg Cys Ser Thr Glu Asp Pro Ala
                845                 850
Asp Cys Pro Pro Asp Pro Thr Tyr Trp Glu Thr Glu
        855                 860
```

CAD7

FIG. 2D

```
Gly Asn Ile Thr Ile His Ile Thr Asp Thr Asn Asn
865                 870                 875
                    CAD8 →
Lys Val Pro Gln Ala Glu Thr Thr Lys Phe Asp Thr
            880                 885
Val Val Tyr Ile Tyr Glu Asn Ala Thr His Leu Asp
    890                 895                 900
Glu Val Val Thr Leu Ile Ala Ser Asp Leu Asp Arg
                905                 910
Asp Glu Ile Tyr His Thr Val Ser Tyr Val Ile Asn
        915                 920
Tyr Ala Val Asn Pro Arg Leu Met Asn Phe Phe Ser
925                 930                 935
Val Asn Arg Glu Thr Gly Leu Val Tyr Val Asp Tyr
            940                 945
Glu Thr Gln Gly Ser Gly Glu Val Leu Asp Arg Asp
    950                 955                 960
Gly Asp Glu Pro Thr His Arg Ile Phe Phe Asn Leu
                965                 970
Ile Asp Asn Phe Met Gly Glu Gly Glu Gly Asn Arg
        975                 980
Asn Gln Asn Asp Thr Glu Val Leu Val Ile  Leu Leu
985                 990                 995
                                    CAD9 →
Asp Val Asn Asp Asn Ala Pro Glu Leu Pro Pro Pro
            1000                1005
Ser Glu Leu Ser Trp Thr Ile Ser Glu Asn Leu Lys
    1010                1015                1020
Gln Gly Val Arg Leu Glu Pro His Ile Phe Ala Pro
                1025                1030
Asp Arg Asp Glu Pro Asp Thr Asp Asn Ser Arg Val
        1035                1040
Gly Tyr Glu Ile Leu Asn Leu Ser Thr Glu Arg Asp
1045                1050                1055
Ile Glu Val Pro Glu Leu Phe Val Met Ile Gln Ile
            1060                1065
Ala Asn Val Thr Gly Glu Leu Glu Thr Ala Met Asp
    1070                1075                1080
```

FIG. 2E

Leu Lys Gly Tyr Trp Gly Thr Tyr Ala Ile His Ile
1085 1090
Arg Ala Phe Asp His Gly Ile Pro Gln Met Ser Met
1095 1100
Asn Glu Thr Tyr Glu Leu Ile Ile His Pro Phe Asn
1105 1110 CAD10 1115
Tyr Tyr Ala Pro Glu Phe Val Phe Pro Thr Asn Asp
1120 1125
Ala Val Ile Arg Leu Ala Arg Glu Arg Ala Val Ile
1130 1135 1140
Asn Gly Val Leu Ala Thr Val Asn Gly Glu Phe Leu
1145 1150
Glu Arg Ile Ser Ala Thr Asp Pro Asp Gly Leu His
1155 1160
Ala Gly Val Val Thr Phe Gln Val Val Gly Asp Glu
1165 1170 1175
Glu Ser Gln Arg Tyr Phe Gln Val Val Asn Asp Gly
1180 1185
Glu Asn Leu Gly Ser Leu Arg Leu Leu Gln Ala Val
1190 1195 1200
Pro Glu Glu Ile Arg Glu Phe Arg Ile Thr Ile Arg
1205 1210
Ala Thr Asp Gln Gly Thr Asp Pro Gly Pro Leu Ser
1215 1220
Thr Asp Met Thr Phe Arg Val Val Phe Val Pro Thr
1225 1230 CAD11 1235
Gln Gly Glu Pro Arg Phe Ala Ser Ser Glu His Ala
1240 1245
Val Ala Phe Ile Glu Lys Ser Ala Gly Met Glu Glu
1250 1255 1260
Ser His Gln Leu Pro Leu Ala Gln Asp Ile Lys Asn
1265 1270
His Leu Cys Glu Asp Asp Cys His Ser Ile Tyr Tyr
1275 1280
Arg Ile Ile Asp Gly Asn Ser Glu Gly His Phe Gly
1285 1290 1295

FIG. 2F

Leu Asp Pro Val Arg Asn Arg Leu Phe Leu Lys Lys
1300 1305
Glu Leu Ile Arg Glu Gln Ser Ala Ser His Thr Leu
1310 1315 1320
Gln Val Ala Ala Ser Asn Ser Pro Asp Gly Gly Ile
1325 1330
Pro Leu Pro Ala Ser Ile Leu Thr Val Thr Val Thr
1335 1340
Val Arg Glu Ala Asp Pro Arg Pro Val Phe Val Arg
1345 1350 1355
Glu Leu Tyr Thr Ala Gly Ile Ser Thr Ala Asp Ser
1360 1365
Ile Gly Arg Glu Leu Leu Arg Leu His Ala Thr Gln
1370 1375 1380
Ser Glu Gly Ser Ala Ile Thr Tyr Ala Ile Asp Tyr
1385 1390
Asp Thr Met Val Val Asp Pro Ser Leu Glu Ala Val
1395 1400
Arg Gln Ser Ala Phe Val Leu Asn Ala Gln Thr Gly
1405 1410 1415
Val Leu Thr Leu Asn Ile Gln Pro Thr Ala Thr Met
1420 1425
His Gly Leu Phe Lys Phe Glu Val Thr Ala Thr Asp
1430 1435 1440
Thr Ala Gly Ala Gln Asp Arg Thr Asp Val Thr Val
1445 1450
Tyr Val Val Ser Ser Gln Asn Arg Val Tyr Phe Val
1455 1460
Phe Val Asn Thr Leu Gln Gln Val Glu Asp Asn Arg
1465 1470 1475
Asp Phe Ile Ala Asp Thr Phe Ser Ala Gly Phe Asn
1480 1485
Met Thr Cys Asn Ile Asp Gln Val Val Pro Ala Asn
1490 1495 1500
Asp Pro Val Thr Gly Val Ala Leu Glu His Ser Thr
1505 1510

FIG. 2G

Gln Met Arg Gly His Phe Ile Arg Asp Asn Val Pro
1515 1520
Val Leu Ala Asp Glu Ile Glu Gln Ile Arg Ser Asp
1525 1530 1535
Leu Val Leu Leu Ser Ler Ile Gln Thr Thr Leu Ala
1540 1545
Ala Arg Ser Leu Val Leu Gln Asp Leu Leu Thr Asn
1550 1555 1560
Ser Ser Pro Asp Ser Ala Pro Asp Ser Ser Leu Thr
1565 1570
Val Thr Val Leu Ala Ser Leu Ser Ala Val Leu Gly
1575 1580
Phe Met Cys Leu Val Leu Leu Leu Thr Phe Ile Ile
1585 1590 1595
Arg Thr Arg Ala Leu Asn Arg Arg Leu Glu Ala Leu
1600 1605
Ser Met Thr Lys Tyr Gly Ser Leu Asp Ser Gly Leu
1610 1615 1620
Asn Arg Ala Gly Ile Ala Ala Pro Gly Thr Asn Lys
1625 1630
His Thr Val Glu Gly Ser Asn Pro Ile Phe Asn Glu
1635 1640
Ala Ile Lys Thr Pro Asp Leu Asp Ala Ile Ser Glu
1645 1650 1655
Gly Ser Asn Asp Ser Asp Leu Ile Gly Ile Glu Asp
1660 1665
Leu Pro His Phe Gly Asn Val Phe Met Asp Pro Glu
1670 1675 1680
Val Asn Glu Lys Ala Asn Gly Tyr Pro Glu Val Ala
1685 1690
Asn His Asn Asn Asn Phe Ala Phe Asn Pro Thr Pro
1695 1700
Phe Ser Pro Glu Phe Val Asn Gly Gln Phe Arg Lys
1705 1710 1715

Ile

FIG. 2H

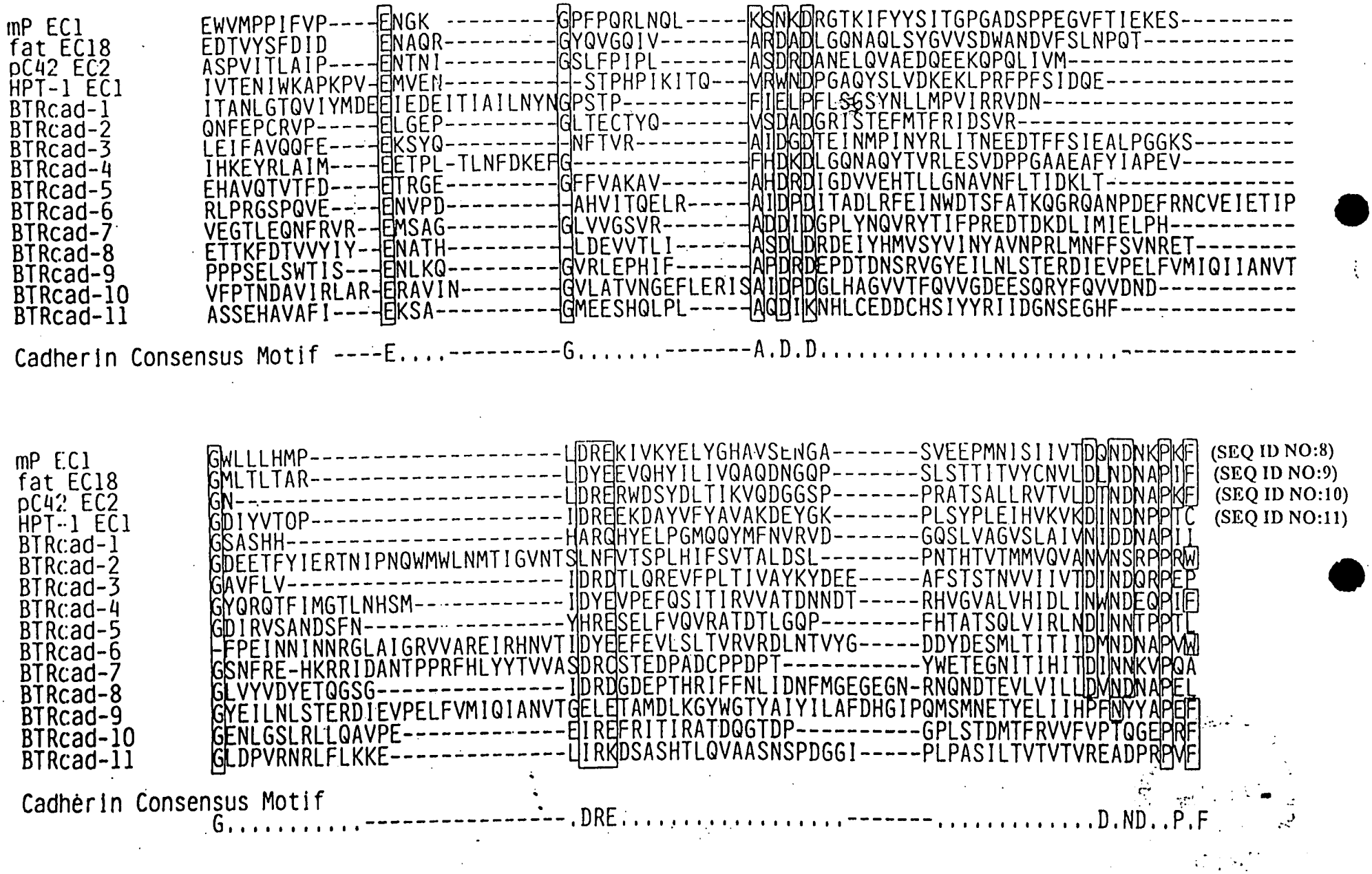
mP EC1
fat EC18
pC42 EC2
HPT-1 EC1
BTRcad-1
BTRcad-2
BTRcad-3
BTRcad-4
BTRcad-5
BTRcad-6
BTRcad-7
BTRcad-8
BTRcad-9
BTRcad-10
BTRcad-11
Cadherin Consensus Motif
(SEQ ID NO:8)
(SEQ ID NO:9)
(SEQ ID NO:10)
(SEQ ID NO:11)

FIG. 2I

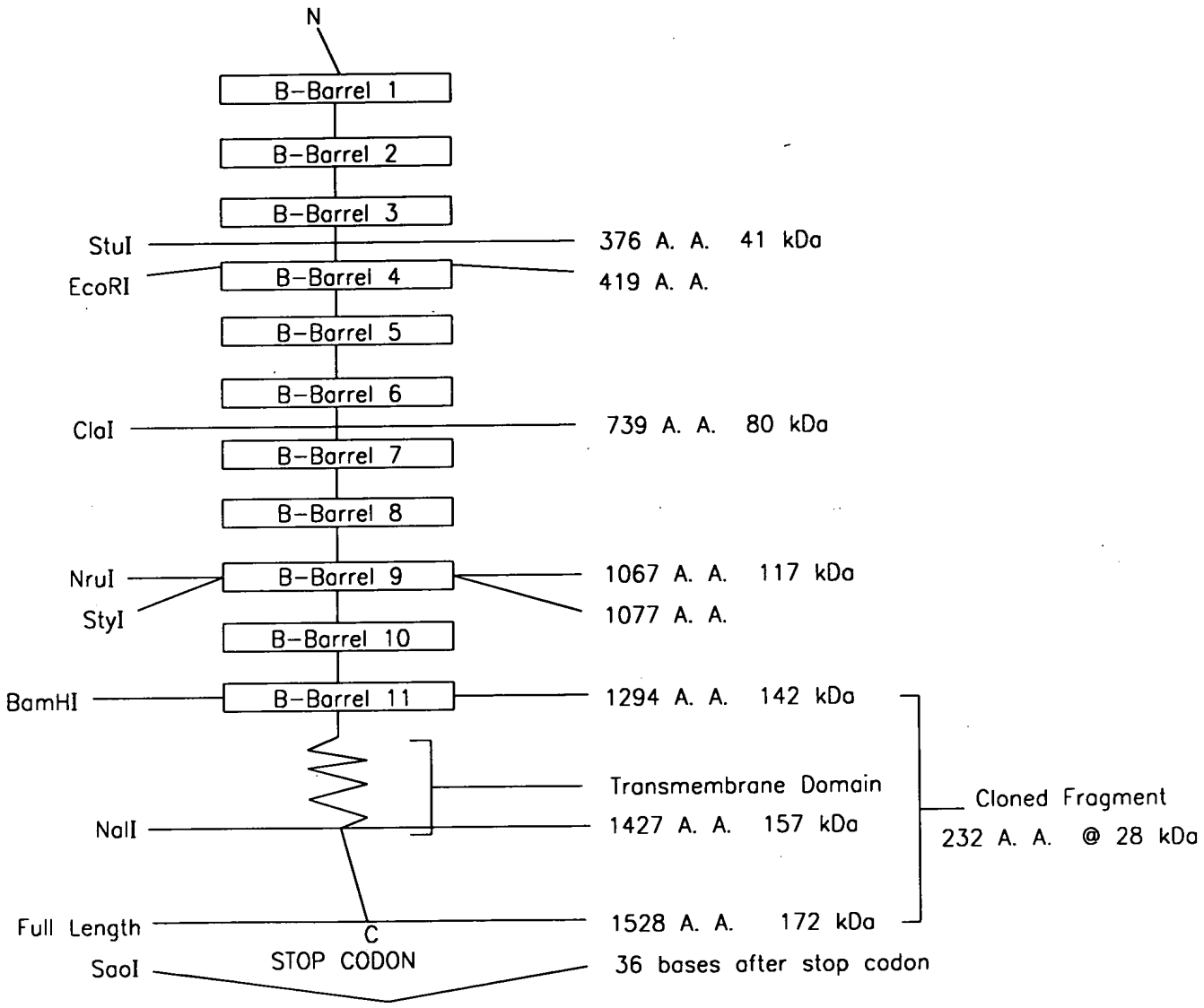
N
B-Barrel 1
B-Barrel 2
B-Barrel 3
StuI
376 A. A. 41 kDa
EcoRI
B-Barrel 4
419 A. A.
B-Barrel 5
B-Barrel 6
ClaI
739 A. A. 80 kDa
B-Barrel 7
B-Barrel 8
NruI
B-Barrel 9
1067 A. A. 117 kDa
StyI
1077 A. A.
B-Barrel 10
BamHI
B-Barrel 11
1294 A. A. 142 kDa
Transmembrane Domain
NaiI
1427 A. A. 157 kDa
Cloned Fragment
232 A. A. @ 28 kDa
Full Length
1528 A. A. 172 kDa
C
STOP CODON
SacI
36 bases after stop codon

FIG. 3

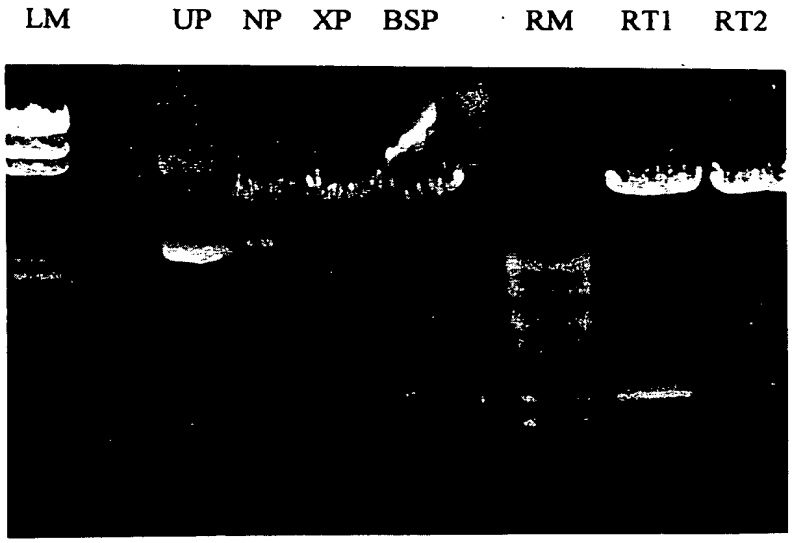

FIG. 4

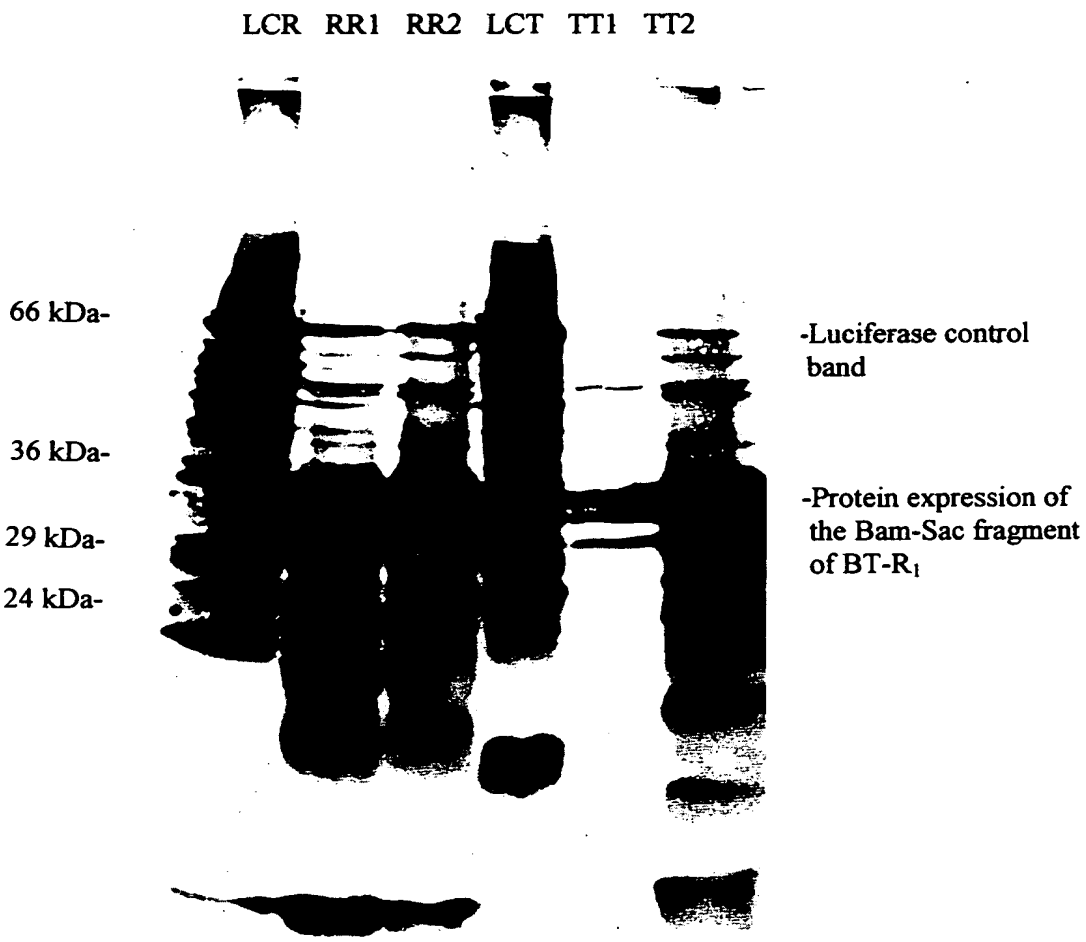
LCR
RR1
RR2
LCT
TT1
TT2
66 kDa-
36 kDa-
29 kDa-
24 kDa-
-Luciferase control band
-Protein expression of the Bam-Sac fragment of BT-R1

FIG. 5

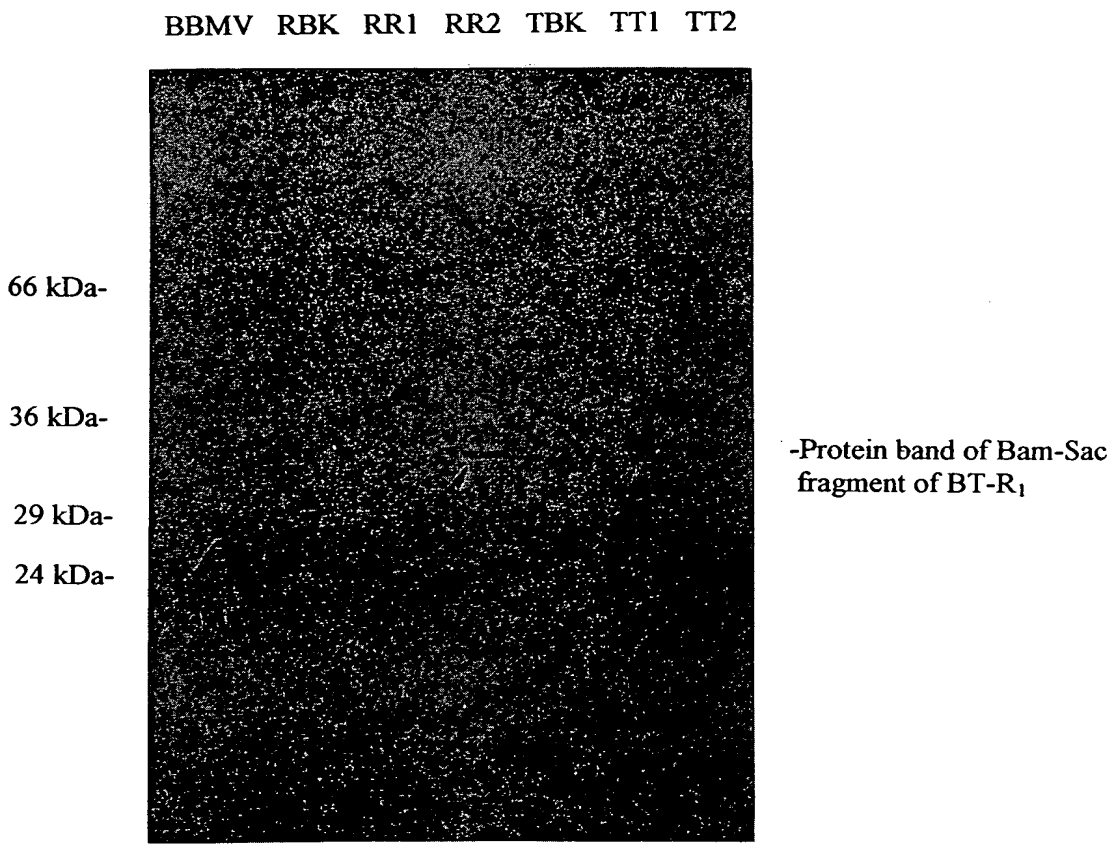
BBMV RBK RR1 RR2 TBK TT1 TT2
66 kDa-
36 kDa-
29 kDa-
24 kDa-
-Protein band of Bam-Sac fragment of BT-R1

FIG. 6

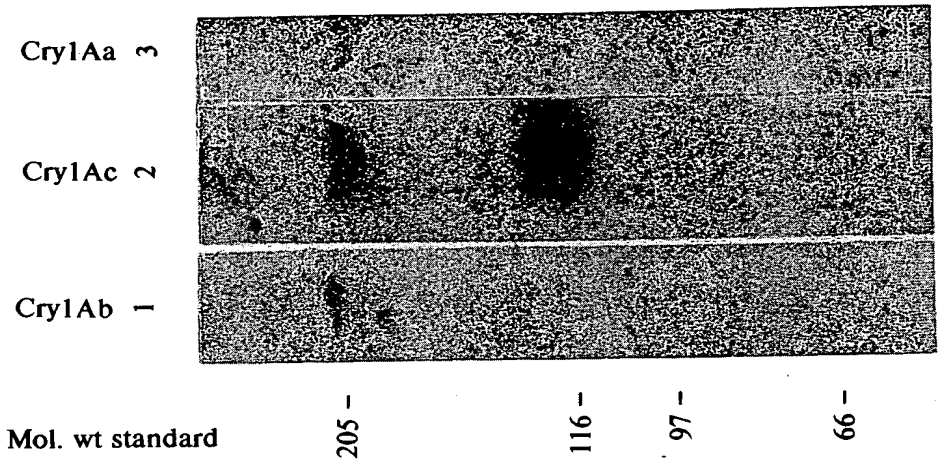
Cry1Aa 3
Cry1Ac 2
Cry1Ab 1
Mol. wt standard
205 –
116 –
97 –
66 –

FIG. 7B

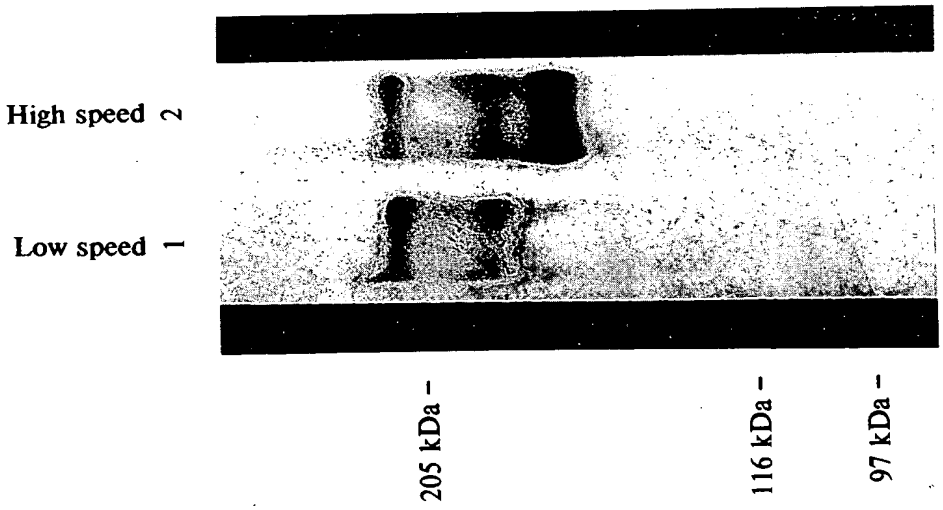
High speed 2
Low speed 1
205 kDa –
116 kDa –
97 kDa –

FIG. 7A

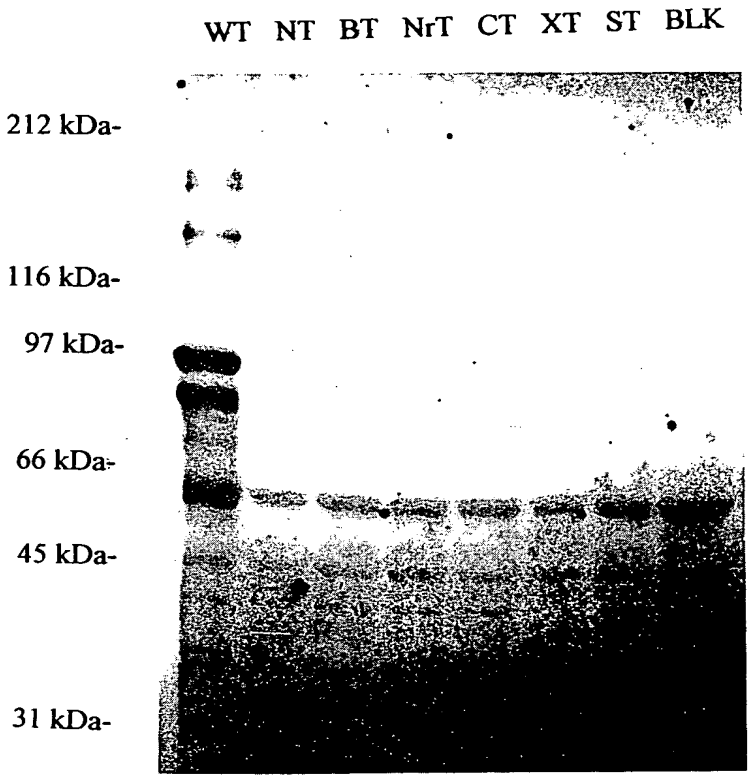
WT NT BT NrT CT XT ST BLK
212 kDa-
116 kDa-
97 kDa-
66 kDa-
45 kDa-
31 kDa-
-Protein band of wild-type full-length BT-R1 expression
-Bands here and below due to RRL binding of Cry1Ab

FIG. 8